The duration, dynamics and determinants of SARS-CoV-2 antibody responses in individual healthcare workers: Supplement

Supplementary methods

PCR platforms

PCR was performed using the Public Health England SARS-CoV-2 assay (targeting the RdRp gene), one of five commercial assays: Abbott RealTime (targeting RdRp and N genes; Abbott, Maidenhead, UK), Altona RealStar (targeting E and S genes; Altona Diagnostics, Liverpool, UK), Cepheid Xpert® Xpress SARS-CoV-2 (targeting N2 and E; Cepheid, California, USA), BioFire® Respiratory 2.1 (RP2.1) panel with SARS-CoV-2 (targeting ORF1ab and ORF8; Biofire diagnostics, Utah, USA), Thermo Fisher TaqPath assay (targeting S and N genes, and ORF1ab; Thermo Fisher, Abingdon, UK) or using the ABI 7500 platform (Thermo Fisher, Abingdon, UK) with the US Centers for Disease Control and Prevention Diagnostic Panel of two probes targeting the N gene.

Statistical methods

We used Bayesian linear mixed models to analyse the duration of antibody responses, starting from each individual's measured maximum antibody level. We assumed antibody levels fell exponentially, and so modelled the log2 transformed antibody level over time. We allowed for correlated random intercept and slope terms to allow for per individual variation. We analysed the univariable effect of covariates of interest on the fixed effect intercept and slope terms, including age, gender, ethnicity, recall of prior symptoms compatible with Covid-19, and a previous positive SARS-CoV-2 PCR test (undertaken either following symptoms or as part of asymptomatic screening). Multivariable models were also fitted, undertaking variable selection based on the leave-one-out cross-validation information criterion (LOOIC), calculated using Pareto smoothed importance sampling, or k-fold cross-validation were Pareto k was >0.7. However, there was no evidence than any model was a better fit than the full multivariable model, and so this is presented. We allowed for non-linear effects of age by using natural cubic splines (R "ns" command) with up to 5 knots

using default locations, choosing the best fitting model based on LOOIC.

Our approach is potentially subject to two biases. The first arises from regression to the mean arising from random measurement error, because the analysis is conditional on starting the with maximum antibody titre. If antibody titres are measured close in time, such that they are in fact stable, then conditioning on starting with the maximum titre will lead to falls being erroneously observed. However, if the antibody titres are measured sufficiently far apart with respect to the rate of change with time this effect will become less important. To quantify this, we performed a sensitivity analysis in which we performed the same analysis, but only considered individuals with at least two antibody results after their maximum result and excluded the initial maximum result. This sensitivity analysis also addresses a second potential bias, where if an individual's maximum antibody titre was measured while their levels were still climbing this may lead to the slope of the decline being under-estimated.

By analysing individuals with a positive PCR test, we additionally modelled the antibody trajectory from a first positive PCR test. We used Bayesian linear mixed models as above but allowed for non-linear effects of time by using natural cubic splines, choosing the number of knots (up to 5) and subsequently their positions based on the LOOIC.

Analyses were performed using R 3.6.3 and the rstanarm library version 2.21.1. For all analyses weakly informative priors were used (see Supplementary Table S1). At least 4 chains were run per analysis to identify the burn-in period and ensure convergence, which was confirmed visually and by ensuring the Gelman-Rubin statistic was <1.1 (actual values are presented). The chains were run for a sufficient length of time to ensure the effective sample size for all parameters exceeded 200. Credibility intervals were calculated using highest posterior density intervals.

We used Bayesian parametric model for interval censored regression (R package, icenReg version 2.0.15) to estimate the proportion of individuals remaining antibody positive at varying times following their maximum test result allowing for the fact that antibody levels are only measured intermittently. The true event time, i.e. the time becoming antibody negative is unobserved, instead, the response interval that the event occurred within was used for the modelling. We used the default Weibull distribution, using weakly informative priors for the log_scale and log_shape

(normal(0, 10)). Convergence and sufficient effective sample sizes were confirmed as above.

Role of the funding source

The funders had no role in study design; in the collection, analysis, and interpretation of data; in the writing of the report; or in the decision to submit the paper for publication.

Supplementary results

Sensitivity analysis

109 participants had ≥2 anti-nucleocapsid IgG readings after their maximum observed antibody titre and were included in a sensitivity analysis to investigate the impact of starting with each individual's maximum result on half-life estimates (which should be independent of starting values under the exponential decay assumption). Using only observations after the maximum antibody titre, the estimated half-life was 83.0 (95%CrI 71.8-97.2) days, consistent with the main analysis, with a lower estimated intercept (2.8 [95%CrI 2.5-3.1]), as expected.

Supplementary tables

Model term	Specified priors	Adjusted priors*
Intercept	normal (1.4, 2.5)	normal (1.4, 2.9)
Coefficient for slope	normal (0,2.5)	normal (0, 0.05)
Coefficient for change in intercept (Male)		normal (0, 6.6)
Coefficient for change in slope (Male)		normal (0, 0.08)
Coefficient for change in intercept (Age)		normal (0, 2.4)
Coefficient for change in slope (Age)		normal (0, 0.01)
Coefficient for change in intercept (Black)		normal (0, 12.3)
Coefficient for change in slope (Black)		normal (0, 0.15)
Coefficient for change in intercept (Asian)		normal (0, 7.2)
Coefficient for change in slope (Asian)		normal (0, 0.08)
Coefficient for change in intercept (Other)		normal (0, 10.5)
Coefficient for change in slope (Other)		normal (0, 0.12)
Coefficient for change in intercept (Prior symptom)		normal (0, 5.8)
Coefficient for change in slope (Prior symptom)		normal (0, 0.05)
Coefficient for change in intercept (PCR-symptomatic)		normal (0, 7.0)
Coefficient for change in slope (PCR-symptomatic)		normal (0, 0.08)
Coefficient for change in intercept (PCR-asymptomatic)		normal (0, 8.5)
Coefficient for change in slope (PCR-asymptomatic)		normal (0, 0.10)
Auxiliary (sigma)	exponential (rate=1)	exponential (rate=0.88)
Covariance	decov (regularization = 1, concentration = 1, shape = 1, scale = 1)	decov (regularization = 1, concentration = 1, shape = 1, scale = 1)

Supplementary Table S1. Priors used in analysis. *rstanarm internally adjusts the scales of the priors to make them weakly informative by default.

		Anti-nucleocapsid				
		Negative	Equivocal	Positive	Not Done	Total
Anti-spike	Negative	2242	41	24	47	2354
	Equivocal	191	7	5	6	209
	Positive	44	36	474	6	560
	Not Done	128	6	19	0	153
	Total	2605	90	522	59	3276

Supplementary Table S2. Individuals with ≥2 samples processed by each immunoassay and the result of the maximum antibody level per individual.

		Posterior mean	Monte-Carlo Standard Error (MCSE)	Posterior standard deviation (SD)	95% Credible interval (CrI)		Effective sample size	Gelman-Rubin statistic (Rhat)
Baseline model	Intercept	2.08917	0.00085	0.03241	2.02481	2.15160	1455	1.00
	t (slope)	-0.01172	0.00001	0.00031	-0.01232	-0.01111	2262	1.00
	Standard deviation of errors (sigma)	0.28047	0.00064	0.01317	0.25588	0.30860	427	1.01
	Random effect intercept standard deviation	0.39783	0.00088	0.03089	0.34109	0.46177	1241	1.00
	Random effect intercept & slope covariance	0.00258	0.00000	0.00024	0.00214	0.00306	2236	1.00
	Random effect slope standard deviation	0.00003	0.00000	0.00000	0.00002	0.00004	952	1.00
Gender model	Intercept: Female	2.08429	0.00113	0.03637	2.01404	2.15667	1031	1.00
	t (slope): Female	-0.01179	0.00001	0.00035	-0.01248	-0.01108	2010	1.00
	Change in intercept: Male	0.00830	0.00227	0.07497	-0.13754	0.15534	1087	1.00
	Change in slope: Male	0.00024	0.00002	0.00073	-0.00116	0.00166	1844	1.00
	Standard deviation of errors (sigma)	0.28035	0.00080	0.01460	0.25264	0.30968	336	1.01
	Random effect intercept standard deviation	0.39923	0.00094	0.03213	0.33895	0.46301	1176	1.00
	Random effect intercept & slope covariance	0.00258	0.00001	0.00025	0.00212	0.00309	1984	1.00
	Random effect slope standard deviation	0.00003	0.00000	0.00000	0.00002	0.00004	696	1.00
Age model	Intercept :41-years old	1.93419	0.00289	0.11256	1.83195	2.03702	1517	1.00

	t (slope): 41-years old	-0.01331	0.00002	0.00107	-0.01434	-0.01228	2439	1.00
	Change in intercept: per 10-year older	0.09246	0.00069	0.02697	0.03743	0.14368	1525	1.00
	Change in slope: per 10-year older	0.00095	0.00001	0.00025	0.00045	0.00144	2466	1.00
	Standard deviation of errors (sigma)	0.27913	0.00080	0.01430	0.25278	0.30950	319	1.01
	Random effect intercept standard deviation	0.38754	0.00095	0.03137	0.33221	0.45420	1092	1.00
	Random effect intercept & slope covariance	0.00246	0.00001	0.00023	0.00201	0.00294	1808	1.00
	Random effect slope standard deviation	0.00003	0.00000	0.00000	0.00002	0.00003	719	1.00
Ethnicity model	Intercept: White	2.00937	0.00116	0.03871	1.93435	2.08513	1109	1.00
	t (slope): White	-0.01229	0.00001	0.00038	-0.01304	-0.01154	1884	1.00
	Change in intercept: Black	0.15572	0.00320	0.13793	-0.11145	0.42489	1854	1.00
	Change in intercept: Asian	0.26813	0.00227	0.08109	0.10807	0.42587	1274	1.00
	Change in intercept: Other	0.19450	0.00311	0.11963	-0.03466	0.42948	1476	1.00
	Change in slope: Black	0.00083	0.00003	0.00137	-0.00193	0.00349	2767	1.00
	Change in slope: Asian	0.00183	0.00002	0.00081	0.00021	0.00340	2376	1.00
	Change in slope: Other	0.00179	0.00002	0.00116	-0.00047	0.00409	2583	1.00
	Standard deviation of errors (sigma)	0.28016	0.00072	0.01385	0.25438	0.30888	371	1.02
	Random effect intercept standard deviation	0.38866	0.00083	0.03110	0.33174	0.45090	1398	1.00
	Random effect intercept & slope covariance	0.00250	0.00000	0.00024	0.00204	0.00298	2469	1.00

	Random effect slope standard deviation	0.00003	0.00000	0.00000	0.00002	0.00004	824	1.01
Prior symptom model	Intercept: No	1.96200	0.00133	0.04976	1.86363	2.05783	1405	1.00
	t (slope): No	-0.01199	0.00001	0.00049	-0.01292	-0.01104	2210	1.00
	Change in intercept: Yes	0.20553	0.00164	0.06471	0.08020	0.33126	1558	1.00
	Change in slope: Yes	0.00040	0.00001	0.00064	-0.00081	0.00162	2237	1.00
	Standard deviation of errors (sigma)	0.27967	0.00100	0.01474	0.25312	0.31050	217	1.03
	Random effect intercept standard deviation	0.38960	0.00104	0.03174	0.33133	0.45671	923	1.01
	Random effect intercept & slope covariance	0.00256	0.00001	0.00024	0.00211	0.00303	2180	1.00
	Random effect slope standard deviation	0.00003	0.00000	0.00000	0.00002	0.00004	492	1.01
PCR model	Intercept: No	2.03221	0.00103	0.03955	1.95242	2.11065	1473	1.00
	t (slope): No	-0.01248	0.00001	0.00039	-0.01325	-0.01173	2362	1.00
	Change in intercept: Symptomatic	0.21074	0.00211	0.07966	0.05619	0.36638	1420	1.00
	Change in intercept: Asymptomatic	0.07506	0.00243	0.09633	-0.11404	0.26730	1567	1.00
	Change in slope: Symptomatic	0.00241	0.00002	0.00078	0.00097	0.00400	2207	1.00
	Change in slope: Asymptomatic	0.00174	0.00002	0.00092	-0.00005	0.00355	2674	1.00
	Standard deviation of errors (sigma)	0.27887	0.00079	0.01420	0.25269	0.30766	324	1.01
	Random effect intercept standard deviation	0.39308	0.00089	0.03153	0.33412	0.45938	1263	1.00
	Random effect intercept & slope covariance	0.00250	0.00001	0.00024	0.00205	0.00299	2095	1.00

	Random effect slope standard deviation	0.00003	0.00000	0.00000	0.00002	0.00004	742	1.00
Multivariable model	Intercept	1.73447	0.00304	0.11633	1.59589	1.87703	1465	1.00
	t (slope)	-0.01433	0.00002	0.00115	-0.01569	-0.01295	2353	1.00
	Change in intercept: Male	-0.02490	0.00187	0.07344	-0.17412	0.11775	1547	1.00
	Change in intercept: per 10-year older	0.08209	0.00073	0.02647	0.02996	0.13387	1314	1.00
	Change in intercept: Black	0.16392	0.00334	0.13832	-0.11071	0.43263	1715	1.00
	Change in intercept: Asian	0.24471	0.00229	0.08123	0.08251	0.40655	1259	1.00
	Change in intercept: Other	0.19820	0.00280	0.11583	-0.03129	0.42335	1712	1.00
	Change in intercept: Had symptom	0.18587	0.00162	0.06487	0.05610	0.30973	1598	1.00
	Change in intercept: Symptomatic PCR	0.13758	0.00230	0.08069	-0.01969	0.29519	1233	1.00
	Change in intercept: Asymptomatic PCR	0.06518	0.00263	0.09549	-0.12199	0.25202	1316	1.00
	Change in slope: Male	-0.00014	0.00001	0.00073	-0.00158	0.00128	2435	1.00
	Change in slope: per 10-year older	0.00089	0.00001	0.00026	0.00036	0.00139	2266	1.00
	Change in slope: Black	0.00056	0.00003	0.00135	-0.00204	0.00321	2501	1.00
	Change in slope: Asian	0.00149	0.00002	0.00081	-0.00011	0.00305	2575	1.00
	Change in slope: Other	0.00187	0.00002	0.00113	-0.00028	0.00407	2572	1.00
	Change in slope: Had symptom	0.00007	0.00001	0.00064	-0.00119	0.00135	2719	1.00
	Change in slope: Symptomatic PCR	0.00217	0.00002	0.00078	0.00059	0.00369	2551	1.00
	Change in slope: Asymptomatic PCR	0.00151	0.00002	0.00089	-0.00023	0.00329	2184	1.00
	Standard deviation of errors (sigma)	0.27831	0.00070	0.01404	0.25289	0.30824	398	1.01

	Random effect intercept standard deviation	0.37052	0.00080	0.03067	0.31432	0.43385	1462	1.00
	Random effect intercept & slope covariance	0.00233	0.00000	0.00023	0.00191	0.00278	2186	1.00
	Random effect slope standard deviation	0.00003	0.00000	0.00000	0.00002	0.00003	765	1.00

Supplementary Table S3. Original model coefficients and MCMC diagnostics for univariable and multivariable models. In the multivariable model the following characteristics are used as baseline: age 41 years, gender female, ethnicity white, no prior symptoms and no positive PCR test.

Indication	Ct value	Platform	Maximum Abbott titre
Asymptomatic	24.8	Abbott RealTime	0.01
Asymptomatic	24.8	Abbott RealTime	0.01
Asymptomatic	31.2	Abbott RealTime	0.01
Asymptomatic	30.6	Altona RealStar	0.01
Asymptomatic	30.1	Abbott RealTime	0.02
Asymptomatic	26.6	Abbott RealTime	0.02
Asymptomatic	26.3	Abbott RealTime	0.02
Asymptomatic	31.2	Abbott RealTime	0.02
Asymptomatic	31.1	Abbott RealTime	0.02
Asymptomatic	30.1	Abbott RealTime	0.02
Asymptomatic	26.0	Abbott RealTime	0.02
Asymptomatic	30.4	Abbott RealTime	0.03
Asymptomatic	37.0	ABI 7500 RealTime	0.03
Asymptomatic	30.0	Abbott RealTime	0.04
Asymptomatic	29.7	Abbott RealTime	0.04
Asymptomatic	31.3	Abbott RealTime	0.04
Asymptomatic	36.3	ABI 7500 RealTime	0.04
Asymptomatic	28.5	Abbott RealTime	0.05
Asymptomatic	26.6	Abbott RealTime	0.06
Asymptomatic	29.6	Abbott RealTime	0.07
Asymptomatic	24.2	Abbott RealTime	0.07
Asymptomatic	10.3	Abbott RealTime	0.07
Asymptomatic	30.2	Abbott RealTime	0.07
Asymptomatic	14.1	Altona RealStar	0.24
Asymptomatic	26.8	Abbott RealTime	0.25
Asymptomatic	37.3	ABI 7500 RealTime	0.3
Asymptomatic	8.8	Abbott RealTime	0.38
Asymptomatic	20.8	Abbott RealTime	0.61
Asymptomatic	21.4	Abbott RealTime	0.61
Asymptomatic	20.6	Abbott RealTime	1.04
Asymptomatic	24.5	Abbott RealTime	1.33
Asymptomatic	30.6	Abbott RealTime	1.36
Asymptomatic	28.9	Abbott RealTime	1.36
Asymptomatic	30.9	Altona RealStar	1.45
Asymptomatic	19.7	Abbott RealTime	1.49
Asymptomatic	27.2	Altona RealStar	1.64
Asymptomatic	24.6	Abbott RealTime	1.7
Asymptomatic	25.3	Abbott RealTime	1.8

Asymptomatic	20.7	Abbott RealTime	1.87
Asymptomatic	13.5	Abbott RealTime	1.95
Asymptomatic	4.0	Abbott RealTime	2.08
Asymptomatic	6.9	Abbott RealTime	2.1
Asymptomatic	27.3	Abbott RealTime	2.13
Asymptomatic	28.8	Abbott RealTime	2.15
Asymptomatic	4.9	Abbott RealTime	2.18
Asymptomatic	29.6	Abbott RealTime	2.3
Asymptomatic	26.8	Altona RealStar	2.32
Asymptomatic	27.4	Abbott RealTime	2.62
Asymptomatic	26.6	Abbott RealTime	2.85
Asymptomatic	22.2	Abbott RealTime	3.03
Asymptomatic	7.3	Abbott RealTime	3.17
Asymptomatic	18.8	Abbott RealTime	3.24
Asymptomatic	26.5	Abbott RealTime	3.39
Asymptomatic	27.2	Abbott RealTime	3.45
Asymptomatic	28.1	Abbott RealTime	3.49
Asymptomatic	28.5	Abbott RealTime	3.51
Asymptomatic	23.3	Abbott RealTime	3.58
Asymptomatic	6.2	Abbott RealTime	3.73
Asymptomatic	25.2	Abbott RealTime	3.82
Asymptomatic	17.4	Abbott RealTime	3.83
Asymptomatic	26.3	Abbott RealTime	3.95
Asymptomatic	26.4	Abbott RealTime	4.11
Asymptomatic	4.1	Abbott RealTime	4.16
Asymptomatic	26.4	Abbott RealTime	4.16
Asymptomatic	26.8	Abbott RealTime	4.23
Asymptomatic	19.2	Abbott RealTime	4.33
Asymptomatic	9.0	Abbott RealTime	4.34
Asymptomatic	11.2	Abbott RealTime	4.39
Asymptomatic	30.3	Abbott RealTime	4.48
Asymptomatic	23.8	Abbott RealTime	4.59
Asymptomatic	29.7	Abbott RealTime	4.6
Asymptomatic	23.2	Abbott RealTime	4.78
Asymptomatic	25.1	Abbott RealTime	4.83
Asymptomatic	5.5	Abbott RealTime	4.86
Asymptomatic	20.9	Abbott RealTime	4.87
Asymptomatic	24.9	Abbott RealTime	4.89
Asymptomatic	24.0	Abbott RealTime	5

Asymptomatic	22.9	Abbott RealTime	5.09
Asymptomatic	16.6	Abbott RealTime	5.15
Asymptomatic	21.1	Abbott RealTime	5.21
Asymptomatic	22.0	Abbott RealTime	5.24
Asymptomatic	24.3	Abbott RealTime	5.33
Asymptomatic	28.0	Abbott RealTime	5.57
Asymptomatic	22.1	Abbott RealTime	5.62
Asymptomatic	21.7	Abbott RealTime	5.63
Asymptomatic	28.2	Abbott RealTime	5.78
Asymptomatic	21.9	Abbott RealTime	5.83
Asymptomatic	26.3	Abbott RealTime	5.92
Asymptomatic	21.9	Abbott RealTime	5.95
Asymptomatic	22.7	Abbott RealTime	6.15
Asymptomatic	23.9	Abbott RealTime	6.37
Asymptomatic	24.1	Abbott RealTime	6.37
Asymptomatic	20.4	Abbott RealTime	6.65
Asymptomatic	21.8	Abbott RealTime	6.78
Asymptomatic	18.7	Altona RealStar	6.82
Asymptomatic	19.0	Abbott RealTime	6.85
Asymptomatic	25.2	Abbott RealTime	6.89
Asymptomatic	15.0	Abbott RealTime	7.03
Asymptomatic	26.9	Abbott RealTime	7.04
Asymptomatic	26.8	Abbott RealTime	7.05
Asymptomatic	26.1	Abbott RealTime	7.19
Asymptomatic	25.4	Abbott RealTime	7.26
Asymptomatic	22.7	Altona RealStar	7.34
Asymptomatic	27.1	Abbott RealTime	7.51
Asymptomatic	23.0	Abbott RealTime	7.55
Asymptomatic	20.1	Abbott RealTime	7.63
Asymptomatic	29.8	Abbott RealTime	7.82
Asymptomatic	25.2	Abbott RealTime	7.83
Symptomatic	31.8	Altona RealStar	0.01
Symptomatic	28.1	Abbott RealTime	0.04
Symptomatic	16.6	Altona RealStar	0.04
Symptomatic	18.4	Abbott RealTime	0.07
Symptomatic	26.3	Altona RealStar	0.09
Symptomatic	9.6	Abbott RealTime	0.19
Symptomatic	22.9	RdRp	0.39
Symptomatic	11.3	Altona RealStar	0.97

Symptomatic	30.5	RdRp	1.12
Symptomatic	23.3	RdRp	1.14
Symptomatic	5.0	Abbott RealTime	1.15
Symptomatic	30.3	RdRp	1.29
Symptomatic	19.5	RdRp	1.43
Symptomatic	29.4	RdRp	1.58
Symptomatic	18.0	RdRp	1.69
Symptomatic	9.8	Abbott RealTime	1.75
Symptomatic	19.1	RdRp	1.85
Symptomatic	5.2	Abbott RealTime	1.86
Symptomatic	19.7	RdRp	1.89
Symptomatic	18.6	Abbott RealTime	2.09
Symptomatic	20.7	RdRp	2.21
Symptomatic	20.1	Abbott RealTime	2.36
Symptomatic	21.6	Abbott RealTime	2.41
Symptomatic	20.4	RdRp	2.49
Symptomatic	32.0	RdRp	2.57
Symptomatic	20.6	RdRp	2.63
Symptomatic	15.7	Altona RealStar	2.76
Symptomatic	21.5	Altona RealStar	2.76
Symptomatic	17.1	RdRp	2.84
Symptomatic	20.7	RdRp	2.9
Symptomatic	18.3	RdRp	3.2
Symptomatic	3.5	Abbott RealTime	3.28
Symptomatic	21.5	RdRp	3.34
Symptomatic	24.2	RdRp	3.52
Symptomatic	9.4	Abbott RealTime	3.63
Symptomatic	17.0	RdRp	3.72
Symptomatic	22.4	RdRp	3.75
Symptomatic	19.0	RdRp	3.79
Symptomatic	20.3	RdRp	3.79
Symptomatic	6.6	Abbott RealTime	3.85
Symptomatic	29.9	RdRp	3.91
Symptomatic	11.8	Abbott RealTime	3.92
Symptomatic	16.7	Altona RealStar	3.93
Symptomatic	25.1	RdRp	4.05
Symptomatic	24.4	RdRp	4.24
Symptomatic	30.3	RdRp	4.29
Symptomatic	17.5	Altona RealStar	4.36

Symptomatic	32.2	RdRp	4.39
Symptomatic	19.7	RdRp	4.48
Symptomatic	19.6	RdRp	4.51
Symptomatic	7.8	Abbott RealTime	4.52
Symptomatic	20.2	RdRp	4.57
Symptomatic	22.1	RdRp	4.77
Symptomatic	35.2	RdRp	4.85
Symptomatic	21.8	RdRp	4.9
Symptomatic	23.5	Altona RealStar	4.91
Symptomatic	25.1	RdRp	4.92
Symptomatic	18.5	Altona RealStar	4.99
Symptomatic	22.7	RdRp	5.04
Symptomatic	27.4	RdRp	5.07
Symptomatic	23.1	Altona RealStar	5.22
Symptomatic	28.8	RdRp	5.24
Symptomatic	18.7	RdRp	5.24
Symptomatic	16.8	RdRp	5.3
Symptomatic	21.8	Abbott RealTime	5.32
Symptomatic	29.7	RdRp	5.33
Symptomatic	25.5	RdRp	5.35
Symptomatic	31.3	RdRp	5.4
Symptomatic	22.8	RdRp	5.43
Symptomatic	21.1	RdRp	5.46
Symptomatic	26.7	RdRp	5.65
Symptomatic	19.7	RdRp	5.65
Symptomatic	26.3	RdRp	5.68
Symptomatic	25.2	Abbott RealTime	5.71
Symptomatic	12.2	Abbott RealTime	5.76
Symptomatic	26.4	RdRp	5.77
Symptomatic	22.5	RdRp	5.77
Symptomatic	20.9	RdRp	5.94
Symptomatic	18.1	RdRp	6
Symptomatic	19.8	RdRp	6.04
Symptomatic	25.1	RdRp	6.07
Symptomatic	27.8	RdRp	6.13
Symptomatic	25.7	RdRp	6.19
Symptomatic	26.6	RdRp	6.25
Symptomatic	21.5	RdRp	6.25
Symptomatic	23.2	RdRp	6.31

Symptomatic	17.9	RdRp	6.31
Symptomatic	22.0	RdRp	6.37
Symptomatic	18.8	RdRp	6.38
Symptomatic	16.0	Abbott RealTime	6.38
Symptomatic	24.3	RdRp	6.4
Symptomatic	21.4	RdRp	6.48
Symptomatic	21.4	RdRp	6.54
Symptomatic	12.3	Abbott RealTime	6.55
Symptomatic	16.7	Abbott RealTime	6.64
Symptomatic	19.6	RdRp	6.66
Symptomatic	21.6	Abbott RealTime	6.69
Symptomatic	18.1	RdRp	6.72
Symptomatic	19.4	RdRp	6.73
Symptomatic	18.9	RdRp	6.78
Symptomatic	26.9	RdRp	6.79
Symptomatic	26.1	Abbott RealTime	6.79
Symptomatic	17.5	RdRp	6.81
Symptomatic	23.5	Altona RealStar	6.82
Symptomatic	25.4	RdRp	6.83
Symptomatic	13.0	Abbott RealTime	6.91
Symptomatic	27.9	RdRp	6.97
Symptomatic	20.3	RdRp	7
Symptomatic	27.7	RdRp	7.04
Symptomatic	30.1	RdRp	7.06
Symptomatic	12.0	Altona RealStar	7.08
Symptomatic	16.7	RdRp	7.24
Symptomatic	19.3	RdRp	7.31
Symptomatic	30.6	RdRp	7.36
Symptomatic	23.2	RdRp	7.39
Symptomatic	36.0	RdRp	7.52
Symptomatic	20.3	RdRp	7.52
Symptomatic	31.5	RdRp	7.58
Symptomatic	36.3	RdRp	7.67
Symptomatic	28.4	RdRp	7.72
Symptomatic	16.8	RdRp	7.78
Symptomatic	23.9	Abbott RealTime	7.85
Symptomatic	19.1	Abbott RealTime	8.08
Symptomatic	19.0	RdRp	8.39

Supplementary Table S4. PCR cycle threshold (Ct) values and corresponding maximum Abbott

CMIA anti-nucleocapsid IgG antibody titres. The Ct values obtained across different platforms are not directly comparable. The median Ct values for the two most commonly used PCR platforms Abbott (n=123) and Public Health England's RdRp assay (n=86) were higher in those who did not seroconvert (maximum antibody titre<1.40) vs. those that did, 26.7 vs. 22.1 (Kruskal-Wallis p=0.0002) and 26.8 vs. 21.9 (p=0.10).

Supplementary File legend

Observed serial anti-nucleocapsid IgG titres are plotted for 452 healthcare workers, timed from the first available antibody result. Antibody results occurring before the maximum titre are shown in blue and were excluded from the fitted model. The fitted model is overlaid, with the posterior mean trajectory indicated by the solid line and the 3 intensities of shaded areas indicating the 50%, 80% and 95% credible intervals.

Supplementary Figures

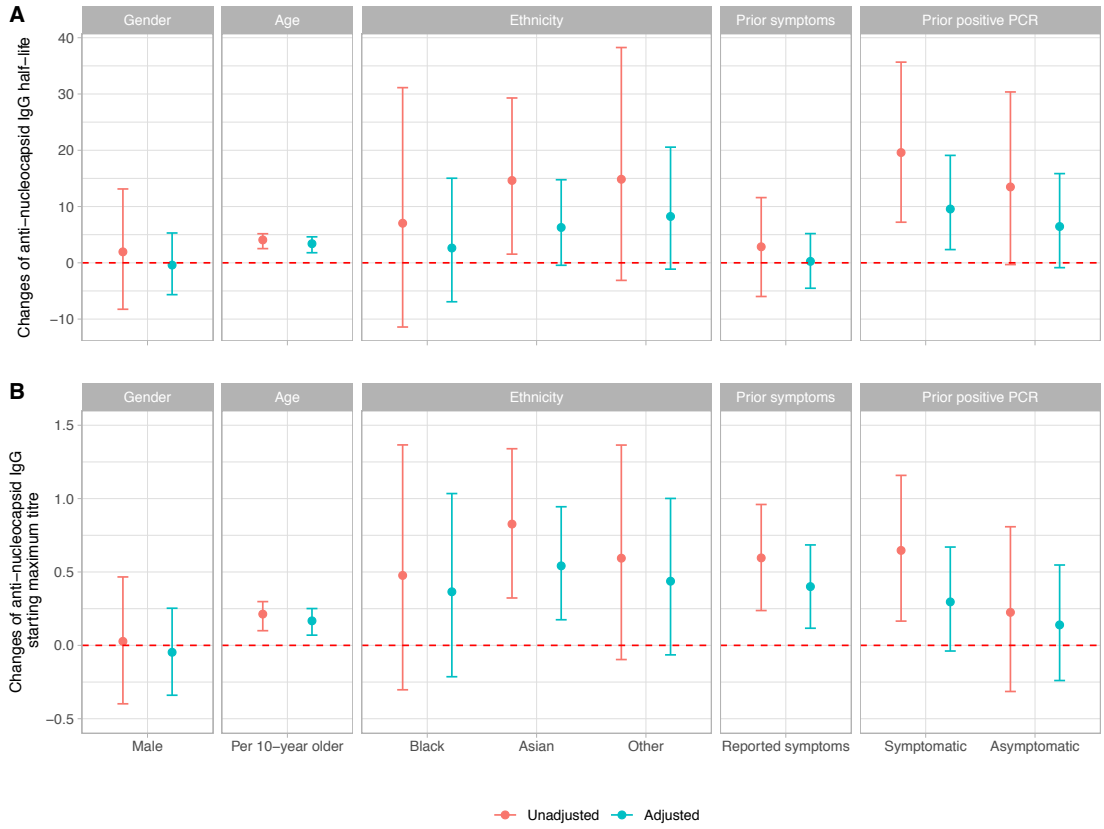

Figure S1. Comparison of the changes of anti-nucleocapsid IgG half-life (Panel A) and starting maximum titre (Panel B) in the univariable (unadjusted) and multivariable (adjusted) models. The baseline group for gender is female, for ethnicity is white, for symptoms is no reported prior symptoms and for prior PCR results is no prior positive. The dashed horizontal line indicates no effect.

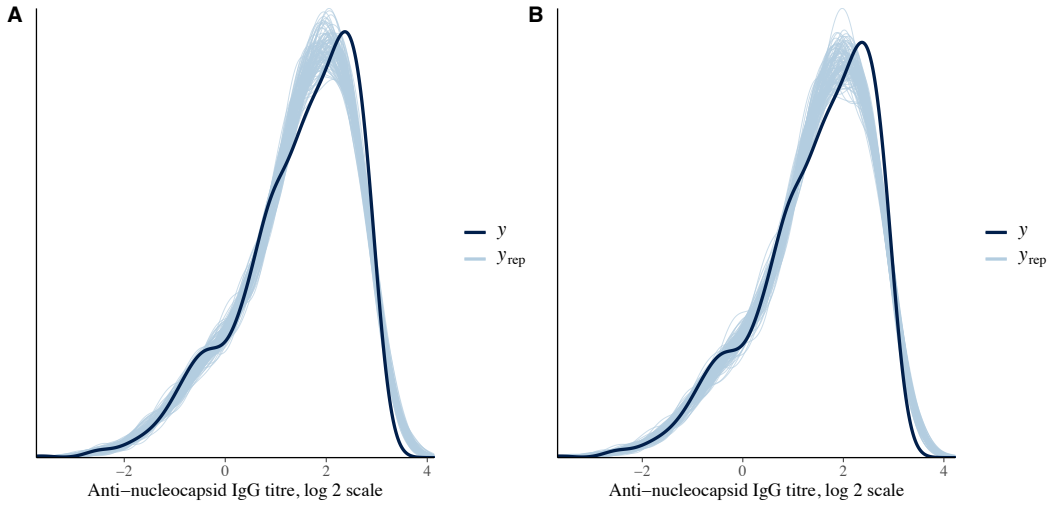

Figure S2. Posterior predictive check for the baseline model (Panel A) and the multivariable model (Panel B). The plot compares the distribution of the observed anti-nucleocapsid IgG titres on a log2 scale (y) and 100 simulated datasets drawn from the posterior predictive distribution (yrep). From the plot, the model is able to generate data that resembles the observed data.

Figure S3. MCMC trace plots for assessing convergence of chains. Panel A shows the trace plots for the baseline model. Panel B shows the trace plots for the multivariable model. In both sets of plots a burn in period of 1000 iterations has been discarded prior to plotting.

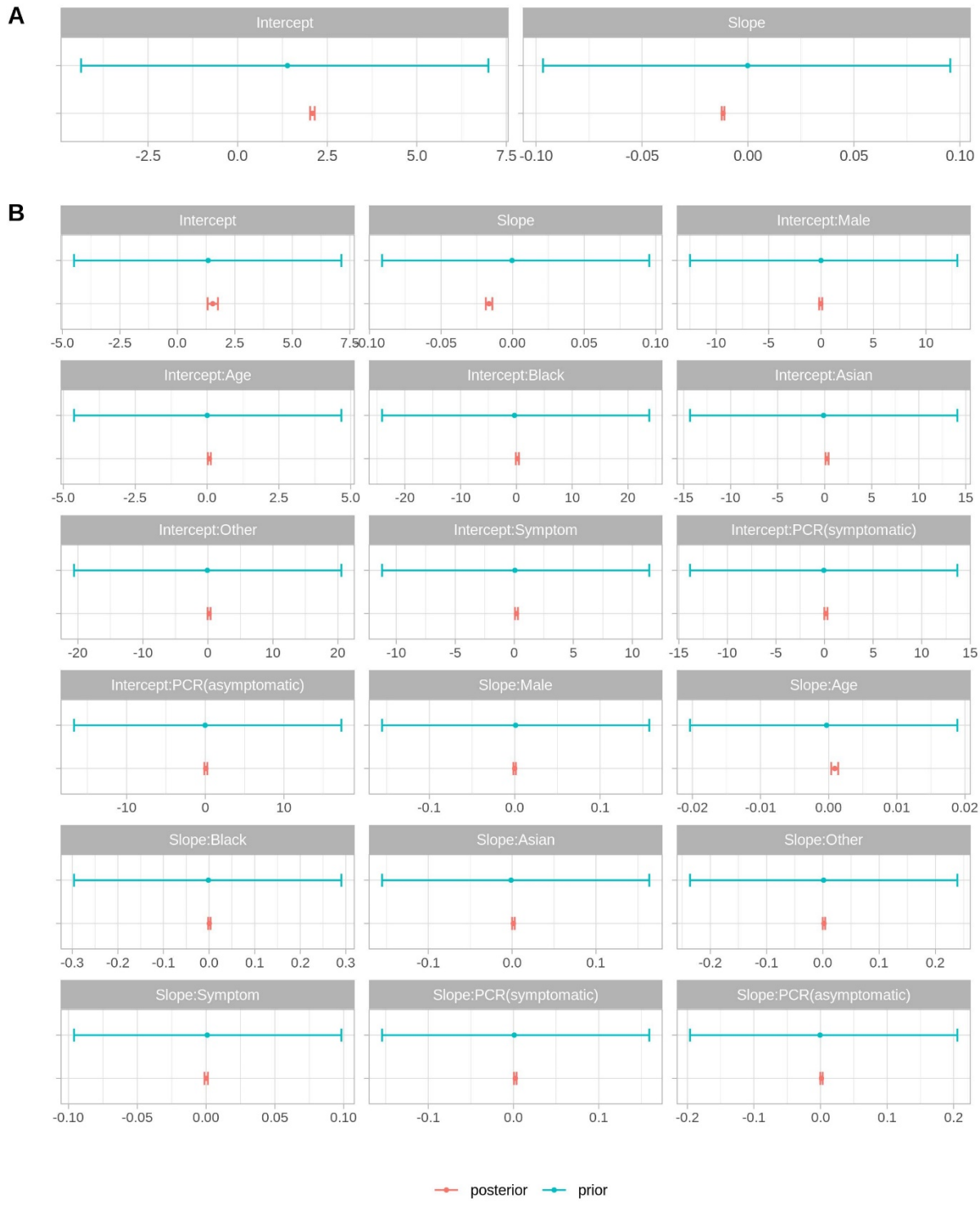

Figure S4. Comparison of the mean and 95% highest density intervals of model parameter prior and posterior distributions. Panel A shows the intercept and slope in the baseline model. Panel B shows the intercept, slope, and covariates coefficients in the multivariable model.

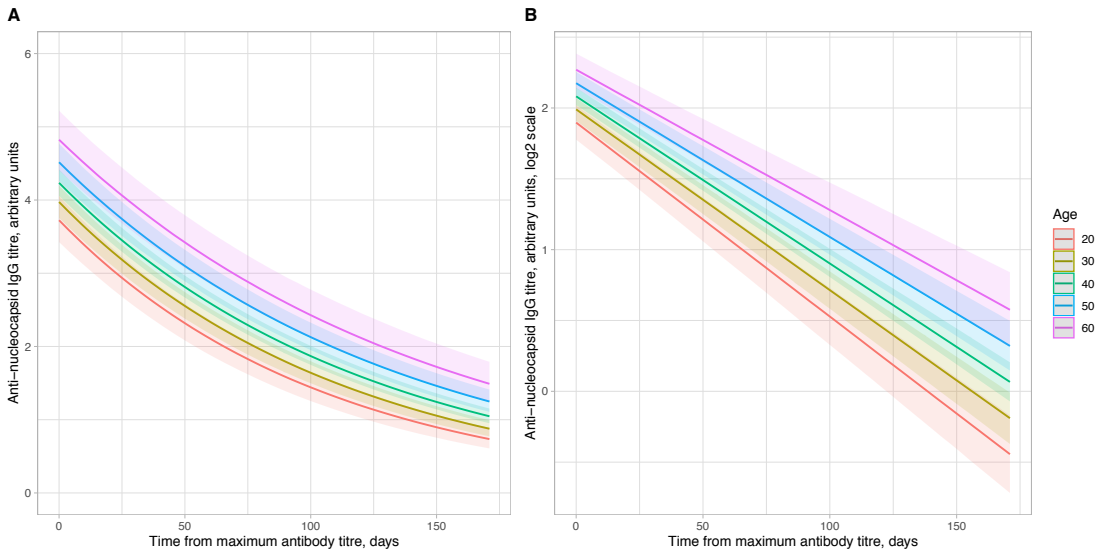

Figure S5. Posterior mean trajectories of anti-nucleocapsid IgG after maximum IgG antibody level by age categories. Panel A shows the relationship on an untransformed scale and Panel B using a log2 scale.

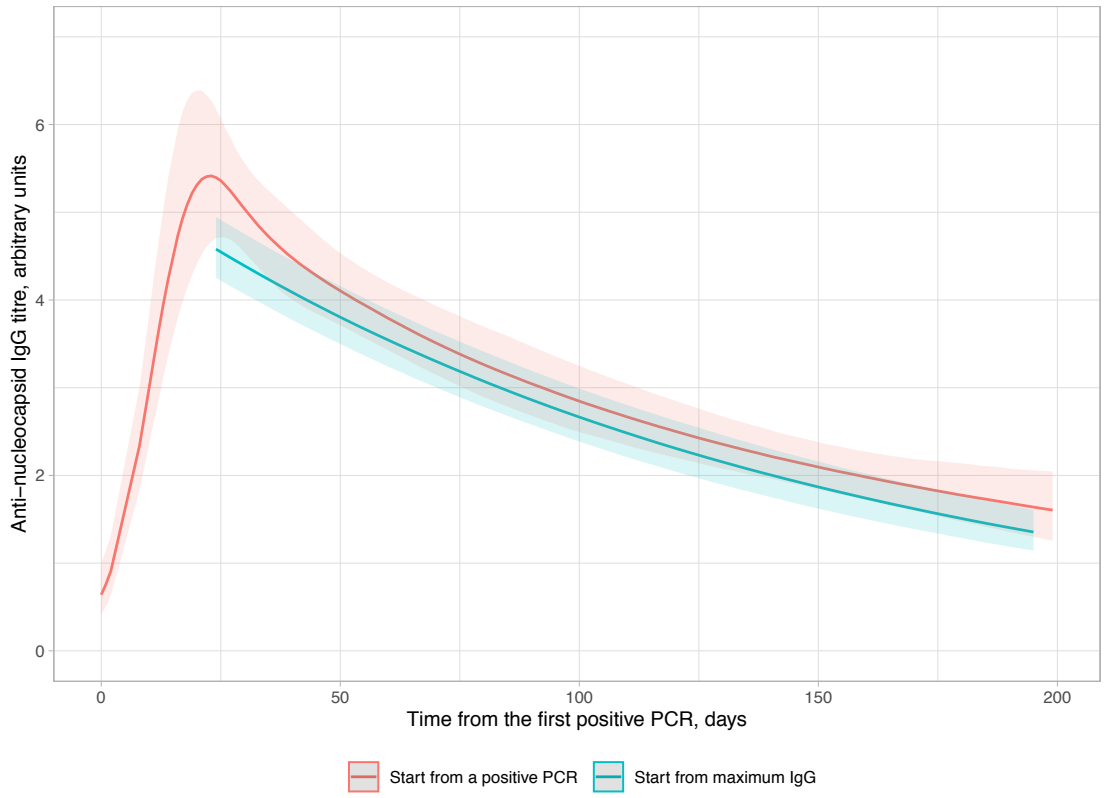

Figure S6. Comparison of anti-nucleocapsid IgG antibody levels following a positive PCR test and the maximum IgG level per individual in those with a positive PCR test. The x-axis value for the model starting from the maximum IgG level is aligned to the maximum point from the model starting with a positive PCR test. The model starting from a positive PCR is fitted with a 5-knot spline (3 interior knots at t=10, t=30, and t=50, locations chosen based on model fit).